

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU, HIROYUKI; MIKI, HIDEO; KAWAI, SHINJI; KIMURA, MICHIO; MATSUMOTO, TOMOAKI; KATSUURA, MIEKO; ENOMOTO, KOICHI; SATOH, YUSUKE
- (ii) TITLE OF INVENTION: A NOVEL PROTEIN AND PROCESS FOR PREPARING THE SAME
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS LLP
 - (B) STREET: 600 THIRD AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/945,459
 - (B) FILING DATE: 09-DEC-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/01062
 - (B) FILING DATE: 19-APR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP7/322403
 - (B) FILING DATE: 17-NOV-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP7/93664
 - (B) FILING DATE: 19-APR-1995
- (vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: CHARLES A. MUSERLIAN
- (B) REGISTRATION NUMBER: 19,683
- (C) REFERENCE/DOCKET NUMBER: 146.1275

- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 661-8000
 - (B) TELEFAX: (212) 661-8002
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PEPTIDE

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMOSAPIENS
 - (F) TISSUE TYPE: FETUS

- (ix) FEATURE:
 - (A) NAME/KEY: MP52
 - (B) LOCATION: 383 TO 501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCA CTG GCC ACT CGC CAG GGC AAG CGA CCC AGC AAG	36
Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys	
1 5 10	
AAC CTT AAG GCT CGC TGC AGT CGG AAG GCA CTG CAT	72
Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His	
15 20	
GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC TGG ATC	108
Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile	
25 30 35	
ATC GCA CCC CTT GAG TAC GAG GCT TTC CAC TGC GAG	144
Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu	
40 45	
GGG CTG TGC GAG TTC CCA TTG CGC TCC CAC CTG GAG	180
Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu	
50 55 60	

CCC ACG AAT CAT GCA GTC ATC CAG ACC CTG ATG AAC 216
Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn
65 70

TCC ATG GAC CCC GAG TCC ACA CCA CCC ACC TGC TGT 252
Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys
75 80

GTG CCC ACG CGA CTG AGT CCC ATC AGC ATC CTC TTC 288
Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
85 90 95

ATT GAC TCT GCC AAC AAC GTG GTG TAT AAG CAG TAT 324
Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr
100 105

GAG GAC ATG GTC GTG GAG TCG TGT GGC TGC AGG 357
Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
110 115

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATAATGCCAC TAGCAACTCG TCAGGGC 27

(3) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTCGACTAC CTGCAGCCAC ACGACT 26